Sequence and assembly of the maize B73 genome.

The Maize Genome Sequencing Consortium. Genome Sequencing Center, Washington University School of Medicine, St. Louis, MO 63108, USA; Arizona Genomics Institute, University of Arizona, Tucson, AZ 85721, USA; Cold Spring Harbor Laboratory, Cold Spring Harbor, NY 11724, USA; and Iowa State University, Ames, IA 50011, USA.

The Maize Genome Sequencing Consortium was launched with a three-year grant to produce the sequence of the maize (B73) genome. We recently completed the sequencing of 16,600 BAC clones that correspond to a minimal tiling path for the genome. These clones represent a near complete genome sequence of maize with unique regions brought to finished quality. This sequence, accessible via GenBank and, of most relevance to cereal geneticists, via a Genome Browser (maizesequence.org), provides a more refined view of the maize genome. In this presentation, we will describe the methods used to select and produce the draft sequence and annotations, as well as efforts being conducted during the third year of the project to improve and annotate the maize genome sequence.

Characterizing the wheat genome by random BAC and sample sequencing.

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The genome structure of the hexaploid wheat cultivar, Chinese Spring (CS), was assayed using several, random-sequencing techniques, including sequencing randomly chosen BACs as well as performing random shotgun Sanger and Next Generation sequencing runs. Twenty-four million bases (9.5X average coverage) of sequence from 220 randomly chosen BACs were generated. More than 10,000 Sanger sequencing reads from the clones of random-sheared genomic DNA produced nearly 8 million bases of sequence. A trial, Applied Biosystems SOLiD run yielded 200 million 35-base reads of which roughly 3 billion bases appear high quality. Furthermore, >190 of the BACs have been successfully mapped using a repeat-junction amplification method on deletion line genomic DNA. Annotation of the first 66 BACs has uncovered 76 confirmed gene homologies, suggesting that there are about 180,000 genes and pseudogenes in CS wheat. Preliminary gene distribution analysis found that 30 of the 66 BACs contained no confirmed genes. These annotation results suggest that one would need to sequence 53% of the CS genome to find 100% of the genes, 49% to find 95% of the genes, or 15% to find 50% of the genes. As expected, the majority of the sequence found in the wheat genome derives from long, terminal repeat (LTR) retrotransposons.